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SEQUENCE LISTING

<110> Berlin, Vivian  
Chiu, Maria Isabel  
Cottarel, Guillaume  
Damagnez, Veronique

<120> IMMUNOSUPPRESSANT TARGET PROTEINS

<130> APBI-P06-036

<140> US 09/517,491

<141> 2000-03-02

<150> US 08/360,144

<151> 1994-12-20

<150> US 08/250,795

<151> 1994-05-27

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 486

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)...(486)

<400> 1

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Leu	Thr	Arg	His	Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	Cys	Glu	
1				5					10					15		

cac	agc	aac	acg	ctg	gtc	cag	cag	gcc	atg	atg	gtg	agt	gaa	gag	ctg	96
His	Ser	Asn	Thr	Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	Glu	Glu	Leu	
			20					25					30			

att	cgg	gta	gcc	atc	ctc	tgg	cat	gag	atg	tgg	cat	gaa	ggc	ctg	gaa	144
Ile	Arg	Val	Ala	Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu	
		35					40					45				

gag	gca	tct	cgc	ttg	tac	ttt	ggg	gag	agg	aac	gtg	aaa	ggc	atg	ttt	192
Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	
	50					55					60					

gag	gtg	ctg	gag	ccc	ctg	cat	gct	atg	atg	gaa	cgg	ggt	ccc	cgg	act	240
Glu	Val	Leu	Glu	Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Arg	Thr	
	65					70				75					80	

ctg	aag	gaa	aca	tcc	ttt	aat	cag	gca	tat	ggc	cga	gat	tta	atg	gag	288
Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	

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85										90					95					
gca	caa	gaa	tgg	tgt	cga	aag	tac	atg	aag	tcg	ggg	aac	gtc	aag	gac	336				
Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	Met	Lys	Ser	Gly	Asn	Val	Lys	Asp					
			100					105					110							
ctc	acg	caa	gcc	tgg	gac	ctc	tac	tat	cac	gtg	ttc	aga	cgg	atc	tca	384				
Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	Tyr	His	Val	Phe	Arg	Arg	Ile	Ser					
		115					120					125								
aag	cag	cta	ccc	cag	ctc	aca	tcc	ctg	gag	ctg	cag	tat	gtg	tcc	ccc	432				
Lys	Gln	Leu	Pro	Gln	Leu	Thr	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro					
	130					135					140									
aaa	ctt	ctg	atg	tgc	cga	gac	ctt	gag	ttg	gct	gtg	cca	gga	aca	tac	480				
Lys	Leu	Leu	Met	Cys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr					
145					150					155					160					
gac	ccc															486				
Asp	Pro																			

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<400> 2

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		20					25					30				
Ile	Arg	Val	Ala	Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu	
	35					40					45					
Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	
50						55				60						
Glu	Val	Leu	Glu	Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Arg	Thr	
65				70						75					80	
Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	
			85						90				95			
Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	Met	Lys	Ser	Gly	Asn	Val	Lys	Asp	
		100					105					110				
Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	Tyr	His	Val	Phe	Arg	Arg	Ile	Ser	
	115					120					125					
Lys	Gln	Leu	Pro	Gln	Leu	Thr	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	
130					135					140						
Lys	Leu	Leu	Met	Cys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	
145				150					155						160	
Asp	Pro															

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<211> 348

<212> DNA

<213> Homo sapiens

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Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp

1

5

10

ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc 97  
Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr  
15 20 25

ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc cgt gac cgt aac 145  
Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn  
30 35 40

aag ccc ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg 193  
Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp  
45 50 55 60

gaa gaa ggg gtt gcc cag atg agt gtg ggt cag cgt gcc aaa ctg act 241  
Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr  
65 70 75

ata tct cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc 289  
Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile  
80 85 90

cca cca cat gcc act ctc gtc ttc gat gtg gag ctt ctaaaactgg 335  
Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu  
95 100

aatgacggga tcc 348

<210> 6

<211> 104

<212> PRT

<213> Homo sapiens

<400> 6

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Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	Leu	Glu
			20				25					30			
Asp	Gly	Lys	Lys	Phe	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	Phe	Lys
		35				40					45				
Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	Gly	Val
	50				55					60					
Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	Pro	Asp
65					70					75				80	
Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	His	Ala
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Thr	Leu	Val	Phe	Asp	Val	Glu	Leu								
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<212> DNA

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<223> oligonucleotide

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48

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<223> oligonucleotide

<400> 8

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34

<210> 9

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide

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1 5 10 15

ctg ggg cac ctg gtc tcc aat gcc ccc cga ctc atc cgc ccc tac atg 96  
Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met  
20 25 30

gag cct att ctg aag gca tta att ttg aaa ctg aaa gat cca gac cct 144  
Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro  
35 40 45

gat cca aac cca ggt gtg atc aat aat gtc ctg gca aca ata gga gaa 192  
Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu  
50 55 60

ttg gca cag gtt agt ggc ctg gaa atg agg aaa tgg gtt gat gaa ctt 240  
Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu  
65 70 75 80

ttt att atc atc atg gac atg ctc cag gat tcc tct ttg ttg gcc aaa 288  
Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys  
85 90 95

agg cag gtg gct ctg tgg acc ctg gga cag ttg gtg gcc agc act ggc 336  
Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly  
100 105 110

tat gta gta gag ccc tac agg aag tac cct act ttg ctt gag gtg cta 384  
Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu  
115 120 125

ctg aat ttt ctg aag act gag cag aac cag ggt aca cgc aga gag gcc 432  
Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala  
130 135 140

atc cgt gtg tta ggg ctt tta ggg gct ttg gat cct tac aag cac aaa 480  
Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys  
145 150 155 160

gtg aac att ggc atg ata gac cag tcc cgg gat gcc tct gct gtc agc 528  
Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser  
165 170 175

ctg tca gaa tcc aag tca agt cag gat tcc tct gac tat agc act agt 576  
Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser

180					185					190						
gaa	atg	ctg	gtc	aac	atg	gga	aac	ttg	cct	ctg	gat	gag	ttc	tac	cca	624
Glu	Met	Leu	Val	Asn	Met	Gly	Asn	Leu	Pro	Leu	Asp	Glu	Phe	Tyr	Pro	
		195					200					205				
gct	gtg	tcc	atg	gtg	gcc	ctg	atg	cgg	atc	ttc	cga	gac	cag	tca	ctc	672
Ala	Val	Ser	Met	Val	Ala	Leu	Met	Arg	Ile	Phe	Arg	Asp	Gln	Ser	Leu	
	210					215					220					
tct	cat	cat	cac	acc	atg	gtt	gtc	cag	gcc	atc	acc	ttc	atc	ttc	aag	720
Ser	His	His	His	Thr	Met	Val	Val	Gln	Ala	Ile	Thr	Phe	Ile	Phe	Lys	
225					230					235					240	
tcc	ctg	gga	ctc	aaa	tgt	gtg	cag	ttc	ctg	ccc	cag	gtc	atg	ccc	acg	768
Ser	Leu	Gly	Leu	Lys	Cys	Val	Gln	Phe	Leu	Pro	Gln	Val	Met	Pro	Thr	
				245					250					255		
ttc	ctt	aat	gtc	att	cga	gtc	tgt	gat	ggg	gcc	atc	cgg	gaa	ttt	ttg	816
Phe	Leu	Asn	Val	Ile	Arg	Val	Cys	Asp	Gly	Ala	Ile	Arg	Glu	Phe	Leu	
			260					265					270			
ttc	cag	cag	ctg	gga	atg	ttg	gtg	tcc	ttt	gtg	aag	agc	cac	atc	aga	864
Phe	Gln	Gln	Leu	Gly	Met	Leu	Val	Ser	Phe	Val	Lys	Ser	His	Ile	Arg	
		275					280					285				
cct	tat	atg	gat	gaa	ata	gtc	acc	ctc	atg	aga	gaa	ttc	tgg	gtc	atg	912
Pro	Tyr	Met	Asp	Glu	Ile	Val	Thr	Leu	Met	Arg	Glu	Phe	Trp	Val	Met	
	290					295					300					
aac	acc	tca	att	cag	agc	acg	atc	att	ctt	ctc	att	gag	caa	att	gtg	960
Asn	Thr	Ser	Ile	Gln	Ser	Thr	Ile	Ile	Leu	Leu	Ile	Glu	Gln	Ile	Val	
305					310					315					320	
gta	gct	ctt	ggg	ggt	gaa	ttt	aag	ctc	tac	ctg	ccc	cag	ctg	atc	cca	1008
Val	Ala	Leu	Gly	Gly	Glu	Phe	Lys	Leu	Tyr	Leu	Pro	Gln	Leu	Ile	Pro	
			325						330					335		
cac	atg	ctg	cgt	gtc	ttc	atg	cat	gac	aac	agc	cca	ggc	cgc	att	gtc	1056
His	Met	Leu	Arg	Val	Phe	Met	His	Asp	Asn	Ser	Pro	Gly	Arg	Ile	Val	
			340					345					350			
tct	atc	aag	tta	ctg	gct	gca	atc	cag	ctg	ttt	ggc	gcc	aac	ctg	gat	1104
Ser	Ile	Lys	Leu	Leu	Ala	Ala	Ile	Gln	Leu	Phe	Gly	Ala	Asn	Leu	Asp	
		355					360					365				
gac	tac	ctg	cat	tta	ctg	ctg	cct	cct	att	gtt	aag	ttg	ttt	gat	gcc	1152
Asp	Tyr	Leu	His	Leu	Leu	Leu	Pro	Pro	Ile	Val	Lys	Leu	Phe	Asp	Ala	
	370					375					380					
cct	gaa	gct	cca	ctg	cca	tct	cga	aag	gca	gcg	cta	gag	act	gtg	gac	1200
Pro	Glu	Ala	Pro	Leu	Pro	Ser	Arg	Lys	Ala	Ala	Leu	Glu	Thr	Val	Asp	
385					390					395					400	
cgc	ctg	acg	gag	tcc	ctg	gat	ttc	act	gac	tat	gcc	tcc	cgg	atc	att	1248
Arg	Leu	Thr	Glu	Ser	Leu	Asp	Phe	Thr	Asp	Tyr	Ala	Ser	Arg	Ile	Ile	
				405					410					415		

cac cct att gtt cga aca ctg gac cag agc cca gaa ctg cgc tcc aca	1296
His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg Ser Thr	
420 425 430	
gcc atg gac acg ctg tct tca ctt gtt ttt cag ctg ggg aag aag tac	1344
Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly Lys Lys Tyr	
435 440 445	
caa att ttc att cca atg gtg aat aaa gtt ctg gtg cga cac cga atc	1392
Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val Arg His Arg Ile	
450 455 460	
aat cat cag cgc tat gat gtg ctc atc tgc aga att gtc aag gga tac	1440
Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile Val Lys Gly Tyr	
465 470 475 480	
aca ctt gct gat gaa gag gag gat cct ttg att tac cag cat cgg atg	1488
Thr Leu Ala Asp Glu Glu Glu Asp Pro Leu Ile Tyr Gln His Arg Met	
485 490 495	
ctt agg agt ggc caa ggg gat gca ttg gct agt gga cca gtg gaa aca	1536
Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr	
500 505 510	
gga ccc atg aag aaa ctg cac gtc agc acc atc aac ctc caa aag gcc	1584
Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala	
515 520 525	
tgg ggc gct gcc agg agg gtc tcc aaa gat gac tgg ctg gaa tgg ctg	1632
Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu	
530 535 540	
aga cgg ctg agc ctg gag ctg ctg aag gac tca tca tcg ccc tcc ctg	1680
Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser Ser Pro Ser Leu	
545 550 555 560	
cgc tcc tgc tgg gcc ctg gca cag gcc tac aac ccg atg gcc agg gat	1728
Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp	
565 570 575	
ctc ttc aat gct gca ttt gtg tcc tgc tgg tct gaa ctg aat gaa gat	1776
Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp	
580 585 590	
caa cag gat gag ctc atc aga agc atc gag ttg gcc ctc acc tca caa	1824
Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln	
595 600 605	
gac atc gct gaa gtc aca cag acc ctc tta aac ttg gct gaa ttc atg	1872
Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met	
610 615 620	
gaa cac agt gac aag ggc ccc ctg cca ctg aga gat gac aat ggc att	1920
Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp Asp Asn Gly Ile	
625 630 635 640	
gtt ctg ctg ggt gag aga gct gcc aag tgc cga gca tat gcc aaa gca	1968
Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala	
645 650 655	

cta cac tac aaa gaa ctg gag ttc cag aaa ggc ccc acc cct gcc att	2016
Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile	
660 665 670	
cta gaa tct ctc atc agc att aat aat aag cta cag cag ccg gag gca	2064
Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala	
675 680 685	
gcg gcc gga gtg tta gaa tat gcc atg aaa cac ttt gga gag ctg gag	2112
Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu Glu	
690 695 700	
atc cag gct acc tgg tat gag aaa ctg cac gag tgg gag gat gcc ctt	2160
Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp Glu Asp Ala Leu	
705 710 715 720	
gtg gcc tat gac aag aaa atg gac acc aac aag gac gac cca gag ctg	2208
Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp Pro Glu Leu	
725 730 735	
atg ctg ggc cgc atg cgc tgc ctc gag gcc ttg ggg gaa tgg ggt caa	2256
Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly Glu Trp Gly Gln	
740 745 750	
ctc cac cag cag tgc tgt gaa aag tgg acc ctg gtt aat gat gag acc	2304
Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val Asn Asp Glu Thr	
755 760 765	
caa gcc aag atg gcc cgg atg gct gct gca gct gca tgg ggt tta ggt	2352
Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala Trp Gly Leu Gly	
770 775 780	
cag tgg gac agc atg gaa gaa tac acc tgt atg atc cct cgg gac acc	2400
Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile Pro Arg Asp Thr	
785 790 795 800	
cat gat ggg gca ttt tat aga gct gtg ctg gca ctg cat cag gac ctc	2448
His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu His Gln Asp Leu	
805 810 815	
ttc tcc ttg gca caa cag tgc att gac aag gcc agg gac ctg ctg gat	2496
Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg Asp Leu Leu Asp	
820 825 830	
gct gaa tta act gca atg gca gga gag agt tac agt cgg gca tat ggg	2544
Ala Glu Leu Thr Ala Met Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly	
835 840 845	
gcc atg gtt tct tgc cac atg ctg tcc gag ctg gag gag gtt atc cag	2592
Ala Met Val Ser Cys His Met Leu Ser Glu Leu Glu Glu Val Ile Gln	
850 855 860	
tac aaa ctt gtc ccc gag cga cga gag atc atc cgc cag atc tgg tgg	2640
Tyr Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp	
865 870 875 880	



gag aga ctg cag ggc tgc cag cgt atc gta gag gac tgg cag aaa atc	2688
Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys Ile	
885 890 895	
ctt atg gtg cgg tcc ctt gtg gtc agc cct cat gaa gac atg aga acc	2736
Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met Arg Thr	
900 905 910	
tgg ctc aag tat gca agc ctg tgc ggc aag agt ggc agg ctg gct ctt	2784
Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg Leu Ala Leu	
915 920 925	
gct cat aaa act tta gtg ttg ctc ctg gga gtt gat ccg tct cgg caa	2832
Ala His Lys Thr Leu Val Leu Leu Leu Gly Val Asp Pro Ser Arg Gln	
930 935 940	
ctt gac cat cct ctg cca aca gtt cac cct cag gtg acc tat gcc tac	2880
Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr	
945 950 955 960	
atg aaa aac atg tgg aag agt gcc cgc aag atc gat gcc ttc cag cac	2928
Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His	
965 970 975	
atg cag cat ttt gtc cag acc atg cag caa cag gcc cag cat gcc atc	2976
Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala Gln His Ala Ile	
980 985 990	
gct act gag gac cag cag cat aag cag gaa ctg cac aag ctc atg gcc	3024
Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala	
995 1000 1005	
cga tgc ttc ctg aaa ctt gga gag tgg cag ctg aat cta cag ggc atc	3072
Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile	
1010 1015 1020	
aat gag agc aca atc ccc aaa gtg ctg cag tac tac agc gcc gcc aca	3120
Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr	
1025 1030 1035 1040	
gag cac gac cgc agc tgg tac aag gcc tgg cat gcg tgg gca gtg atg	3168
Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met	
1045 1050 1055	
aac ttc gaa gct gtg cta cac tac aaa cat cag aac caa gcc cgc gat	3216
Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp	
1060 1065 1070	
gag aag aag aaa ctg cgt cat gcc agc ggg gcc aac atc acc aac gcc	3264
Glu Lys Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala	
1075 1080 1085	
acc act gcc gcc acc acg gcc gcc act gcc acc acc act gcc agc acc	3312
Thr Thr Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Thr Ala Ser Thr	
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Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val	
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Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr	
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Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met	
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Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln	
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Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His	
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Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu	
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Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp	
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Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile	
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Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala	
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Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr	
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Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly	
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Trp	

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 Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys  
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 Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly  
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 Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu  
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 Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu  
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 Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys  
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 Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr  
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 Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met  
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 Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro  
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 His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val  
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 Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp  
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 Asp Tyr Leu His Leu Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala  
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 Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp  
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His	Pro	Ile	Val	Arg	Thr	Leu	Asp	Gln	Ser	Pro	Glu	Leu	Arg	Ser	Thr
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Gln	Ile	Phe	Ile	Pro	Met	Val	Asn	Lys	Val	Leu	Val	Arg	His	Arg	Ile
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Asp	Ile	Ala	Glu	Val	Thr	Gln	Thr	Leu	Leu	Asn	Leu	Ala	Glu	Phe	Met
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Glu	His	Ser	Asp	Lys	Gly	Pro	Leu	Pro	Leu	Arg	Asp	Asp	Asn	Gly	Ile
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Val	Leu	Leu	Gly	Glu	Arg	Ala	Ala	Lys	Cys	Arg	Ala	Tyr	Ala	Lys	Ala
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Leu	His	Tyr	Lys	Glu	Leu	Glu	Phe	Gln	Lys	Gly	Pro	Thr	Pro	Ala	Ile
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Leu	Glu	Ser	Leu	Ile	Ser	Ile	Asn	Asn	Lys	Leu	Gln	Gln	Pro	Glu	Ala
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Ala	Ala	Gly	Val	Leu	Glu	Tyr	Ala	Met	Lys	His	Phe	Gly	Glu	Leu	Glu
	690					695					700				
Ile	Gln	Ala	Thr	Trp	Tyr	Glu	Lys	Leu	His	Glu	Trp	Glu	Asp	Ala	Leu
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Val	Ala	Tyr	Asp	Lys	Lys	Met	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Glu	Leu
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Met	Leu	Gly	Arg	Met	Arg	Cys	Leu	Glu	Ala	Leu	Gly	Glu	Trp	Gly	Gln
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Leu	His	Gln	Gln	Cys	Cys	Glu	Lys	Trp	Thr	Leu	Val	Asn	Asp	Glu	Thr
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His	Asp	Gly	Ala	Phe	Tyr	Arg	Ala	Val	Leu	Ala	Leu	His	Gln	Asp	Leu
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Tyr	Lys	Leu	Val	Pro	Glu	Arg	Arg	Glu	Ile	Ile	Arg	Gln	Ile	Trp	Trp	865	870	875	880
Glu	Arg	Leu	Gln	Gly	Cys	Gln	Arg	Ile	Val	Glu	Asp	Trp	Gln	Lys	Ile		885	890	895
Leu	Met	Val	Arg	Ser	Leu	Val	Val	Ser	Pro	His	Glu	Asp	Met	Arg	Thr	900	905	910	
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Met	Lys	Asn	Met	Trp	Lys	Ser	Ala	Arg	Lys	Ile	Asp	Ala	Phe	Gln	His	965	970	975	
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Gln	Leu	Ile	Ala	Arg	Ile	Asp	Thr	Pro	Arg	Pro	Leu	Val	Gly	Arg	Leu	1205	1210	1215	
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 catgctcaag atttgggaatt ggctgtacca ggtacttacc aagcaggcaa acctgtgac 540  
 agaataatca aatttgatcc tactttttcg attatttcat ctaaacaag accgagaaaa 600  
 ttatcgtgca gaggaagtga tggtaaagac taccaatatg cgttgaaagg acatgaagat 660  
 atcagacaag ataacttagt gatgcaattg tttggtttgg ttaatacgtt gttggtaaat 720  
 gatccggtat gtttcaagag acatttggat atacaacaat atcctgctat tccattatca 780  
 ccaaaagtgg gattgcttgg ttgggttcca aatagtgaca ctttccatgt attgatcaaa 840  
 ggctatcgcg aatcaagaag tataatgttg aatattgaac acaggctttt gttgcaaagt 900  
 gcacctgatt atgatttctt gacattattg caaaaagttg aagtgttcac aagtgcaatg 960  
 gataattgta agggacagga tttgtacaaa gtgttatggc tcaaactctaa atcatccgag 1020  
 gcgtggttgg accgtagaac aacatacacg agatcattag ctgtaatgtc tatggttggg 1080  
 tatatattag gtttggggga taggcacca tcaaatttga tgttggaccg tattactggg 1140  
 aaagtcatcc atattgattt cggagactgt tttgaagcag caatattacg tgagaagtat 1200  
 ccagagagag ttccgttttag attgacgaga atgcttaatt atgccatgga agttagtggg 1260  
 atagagggct cgttcagaat cacatgtgaa catgttatga ggggtgtgag tgataataaa 1320  
 gagtctttta tggcaatatt agaggccttt gcttacgac ccttgataaa ttgggggttt 1380  
 gatttcccaa caaaggcggt ggctgaatca acgggtatac gtgttccaca agtcaacact 1440  
 gcagaattat tacgcagagg acagattgac gaaaaagaag ctgtaagatt gcaaaagcaa 1500  
 aatgaattgg aaataagaaa cgctagagct gcattagtgt tgaaacgtat taccgataag 1560  
 ttaactggta acgatatcaa acggttgaga ggattagatg tgcctactca agtcgataaa 1620  
 ttgattcaac aagccaccag tgttgagaat ttgtgtcagc attacattgg ttgggtgttcg 1680  
 tgttggtagg ttgattatcg tcatgtgtcg ataagtatgg tattgtggta actattttat 1740  
 aaagggaaat attaaagaat tgtatattat taaaaaaaaa aaaaaaaact cgag 1794

<210> 14  
 <211> 562  
 <212> PRT  
 <213> C. albicans

<400> 14  
 Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg  
 1 5 10 15  
 Lys Lys Ala Ala Gln Ser Ile Ile Glu Lys Met Arg Val His Ser Pro  
 20 25 30  
 Ser Leu Val Asp Gln Ala Glu Leu Val Ser Arg Glu Leu Ile Arg Val  
 35 40 45  
 Ala Val Leu Trp His Glu Gln Trp His Asp Ala Leu Glu Asp Ala Ser  
 50 55 60  
 Arg Phe Phe Phe Gly Glu His Asn Thr Glu Lys Met Phe Glu Thr Leu  
 65 70 75 80

Glu	Pro	Leu	His	Gln	Met	Leu	Gln	Lys	Gly	Pro	Glu	Thr	Met	Arg	Glu
			85						90					95	
Gln	Ala	Phe	Ala	Asn	Ala	Phe	Gly	Arg	Glu	Leu	Thr	Asp	Ala	Tyr	Glu
		100					105						110		
Trp	Val	Leu	Asn	Phe	Arg	Arg	Thr	Lys	Asp	Ile	Thr	Asn	Leu	Asn	Gln
	115						120					125			
Ala	Trp	Asp	Ile	Tyr	Tyr	Asn	Val	Phe	Arg	Arg	Val	Ser	Lys	Gln	Val
	130					135					140				
Gln	Leu	Leu	Ala	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	Asp	Leu	Glu
145				150						155				160	
His	Ala	Gln	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	Gln	Ala	Gly
			165						170					175	
Lys	Pro	Val	Ile	Arg	Ile	Ile	Lys	Phe	Asp	Pro	Thr	Phe	Ser	Ile	Ile
		180						185					190		
Ser	Ser	Lys	Gln	Arg	Pro	Arg	Lys	Leu	Ser	Cys	Arg	Gly	Ser	Asp	Gly
	195						200					205			
Lys	Asp	Tyr	Gln	Tyr	Ala	Leu	Lys	Gly	His	Glu	Asp	Ile	Arg	Gln	Asp
	210					215					220				
Asn	Leu	Val	Met	Gln	Leu	Phe	Gly	Leu	Val	Asn	Thr	Leu	Leu	Val	Asn
225				230						235					240
Asp	Pro	Val	Cys	Phe	Lys	Arg	His	Leu	Asp	Ile	Gln	Gln	Tyr	Pro	Ala
			245						250					255	
Ile	Pro	Leu	Ser	Pro	Lys	Val	Gly	Leu	Leu	Gly	Trp	Val	Pro	Asn	Ser
		260					265						270		
Asp	Thr	Phe	His	Val	Leu	Ile	Lys	Gly	Tyr	Arg	Glu	Ser	Arg	Ser	Ile
		275					280					285			
Met	Leu	Asn	Ile	Glu	His	Arg	Leu	Leu	Leu	Gln	Met	Ala	Pro	Asp	Tyr
	290					295					300				
Asp	Phe	Leu	Thr	Leu	Leu	Gln	Lys	Val	Glu	Val	Phe	Thr	Ser	Ala	Met
305				310						315					320
Asp	Asn	Cys	Lys	Gly	Gln	Asp	Leu	Tyr	Lys	Val	Leu	Trp	Leu	Lys	Ser
			325						330					335	
Lys	Ser	Ser	Glu	Ala	Trp	Leu	Asp	Arg	Arg	Thr	Thr	Tyr	Thr	Arg	Ser
		340					345						350		
Leu	Ala	Val	Met	Ser	Met	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Gly	Asp	Arg
	355						360					365			
His	Pro	Ser	Asn	Leu	Met	Leu	Asp	Arg	Ile	Thr	Gly	Lys	Val	Ile	His
	370					375					380				
Ile	Asp	Phe	Gly	Asp	Cys	Phe	Glu	Ala	Ala	Ile	Leu	Arg	Glu	Lys	Tyr
385				390						395					400
Pro	Glu	Arg	Val	Pro	Phe	Arg	Leu	Thr	Arg	Met	Leu	Asn	Tyr	Ala	Met
			405						410					415	
Glu	Val	Ser	Gly	Ile	Glu	Gly	Ser	Phe	Arg	Ile	Thr	Cys	Glu	His	Val
		420						425					430		
Met	Arg	Val	Leu	Arg	Asp	Asn	Lys	Glu	Ser	Leu	Met	Ala	Ile	Leu	Glu
	435					440						445			
Ala	Phe	Ala	Tyr	Asp	Pro	Leu	Ile	Asn	Trp	Gly	Phe	Asp	Phe	Pro	Thr
	450					455					460				
Lys	Ala	Leu	Ala	Glu	Ser	Thr	Gly	Ile	Arg	Val	Pro	Gln	Val	Asn	Thr
465				470						475					480
Ala	Glu	Leu	Leu	Arg	Arg	Gly	Gln	Ile	Asp	Glu	Lys	Glu	Ala	Val	Arg
			485						490					495	
Leu	Gln	Lys	Gln	Asn	Glu	Leu	Glu	Ile	Arg	Asn	Ala	Arg	Ala	Ala	Leu
		500						505					510		
Val	Leu	Lys	Arg	Ile	Thr	Asp	Lys	Leu	Thr	Gly	Asn	Asp	Ile	Lys	Arg
	515						520					525			
Leu	Arg	Gly	Leu	Asp	Val	Pro	Thr	Gln	Val	Asp	Lys	Leu	Ile	Gln	Gln
	530					535					540				

Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser  
 545 550 555 560  
 Cys Trp

<210> 15  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
 gttagtcacg agttgatcag agtagccggt ctatggcacg aattatggta tgaaggactg 60  
 gaagatgcga gccgccaatt tttcgttgaa cataacatag aaaaaatggt ttctacttta 120  
 gaacctttac ataaacactt aggcaatgag cctcaaactg taagtggagt atcgtttcag 180  
 aaatcatttg gtagagattt gaacgatgcc tacgaatggg tgaataacta caaaaagtca 240  
 aaagacatca ataatttgaa ccaagcttgg gatatttatt ataacgtctt cagaaaaata 300  
 acacgtcaaa taccacagtt acaaacctta gacttacagc atgtttctcc ccagcttctg 360  
 gctactcatg atctcgaatt ggctgttcct gggacatat 399

<210> 16  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Val Ser His Glu Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp  
 1 5 10 15  
 Tyr Glu Gly Leu Glu Asp Ala Ser Arg Gln Phe Phe Val Glu His Asn  
 20 25 30  
 Ile Glu Lys Met Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly  
 35 40 45  
 Asn Glu Pro Gln Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly  
 50 55 60  
 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser  
 65 70 75 80  
 Lys Asp Ile Asn Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val  
 85 90 95  
 Phe Arg Lys Ile Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu  
 100 105 110  
 Gln His Val Ser Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala  
 115 120 125  
 Val Pro Gly Thr Tyr  
 130

<210> 17  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 gtcagccacg aattgatacg tatggcgggt ctttggcatg agcaatggta tgagggtctg 60  
 gatgacgcca gtaggcagtt ttttgagaga cataataccg aaaaaatggt tgctgcttta 120  
 gaggctctgt acgaaatgct gaagagagga ccggaaactt tgagggaaat atcgttccaa 180  
 aattcttttg gtagggactt gaatgacgct tacgaatggc tgatgaatta caaaaaatct 240  
 aaagatgtta gtaattttaa ccaagcgtgg gacatttact ataatgtttt caggaaaatt 300  
 ggtaaacagt tgccacaatt acaaactctt gaactacaac atgtgtcgcc aaaactacta 360  
 tctgcgcatg atttggaatt ggctgtcccc gggaccgtg 399

<210> 18  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp  
 1 5 10 15  
 Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn  
 20 25 30  
 Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys  
 35 40 45  
 Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly  
 50 55 60  
 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser  
 65 70 75 80  
 Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val  
 85 90 95  
 Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu  
 100 105 110  
 Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala  
 115 120 125  
 Val Pro Gly Thr Arg  
 130

<210> 19  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 59, 64, 72, 74, 89, 94, 101, 137, 158, 175, 190, 201, 207,  
 210, 213, 218, 234, 243, 257, 283, 286, 289, 292, 314, 325,  
 328, 335, 352, 361, 380, 384, 390, 393, 403, 411, 413, 427,  
 432, 435, 440, 443, 450, 452, 460, 465, 480, 482, 486  
 <223> n = A,T,C or G

<221> misc\_feature  
 <222> 492, 515  
 <223> n = A,T,C or G

<400> 19  
 tgaccctcac cccttcacc tatcccaaaa acctcactgg gtctgtggac aaacaacana 60  
 aatnttttcc ananaggccc caaatgagnc ccangggctc ntcttccatc agaccagtg 120  
 attctgcgac tcacacnctt caattcaaga cctgaccnct agtagggagg ttantcaga 180  
 tcgctggcan cctcggctga ncagatncan agnggggntc gctgttcagt gggncacccc 240  
 tcnctggcct tcttcancag gggctctggga tgttttcagt ggnccnaana cnctgtttag 300  
 agccagggct cagnaaacag aaaanctntc atggnggttc tggacacagg gnaggtctgg 360  
 nacatattgg ggattatgan cagnaccaan acnccactaa atnccccaag nanaaagtgt 420  
 aacctnttct anacnccatn ttntatcagn anaaattttt ttccnataaa tgacatcagn 480  
 antttnaaca tnaaaaaaaaa aaaaaaaaaa aaaaanaaaaa aaaaaaaaaa a 531

<210> 20  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<400> 20  
 gcgtataacg cgtttggaat cactacaggg atgtttaata ccactacaat ggatgatgta 60  
 tataactatc tattcgatga tgaagatacc ccaccaaacc caaaaaaaga gatctggaat 120  
 tcggatcctc gagagatcta tgaatcgtag atactgaaaa accccgcaag ttcacttcaa 180  
 ctgtgcatcg tgcaccatct caatttcttt catttataca tcgttttgcc t 231

<210> 21  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 21  
 tgaagatacc ccaccaaacc c 21

<210> 22  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 22  
 tgcacagttg aagtgaac 18

<210> 23  
 <211> 662  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc feature  
 <222> 27, 373, 443, 461, 483, 485, 507, 583, 588, 593, 605, 606,  
 607, 612, 624, 625, 626, 627, 628, 630, 631, 632, 635, 639,  
 646, 652, 659, 661  
 <223> n = A,T,C or G

<400> 23  
 accaaaccca aaaaaagaga tcctagnaac tagtggatcc cccgggctgc aggaattcgg 60  
 tacgagtcgc cctcagcaga ctgcccagg agaggaaagc atggaggaaa gaccacccat 120  
 ttggtttcgt ggctgtccca acaaaaaatc ccgatggcac gatgaacctc atgaactggg 180  
 agtgcgccat tccaggaaag aaagggactc cgtgggaagg aggcttggtt aaactacgga 240  
 tgcttttcaa agatgattat ccattctcgc caccaaatg taaattcgaa ccaccattat 300  
 ttcacccgaa tgtgtaccct tcggggacag tgtgcctgtc catcttagag gaggacaagg 360  
 actggagggc agncatcaca atcaaacagg atcctattag gaatacagga actttctaaa 420  
 tgaaccaaat atccaagacc agntcaagca gagggctaca ngatttactg ccaaaacaga 480  
 gtngngtacg agaaagggtc cgagcanagc cagaagtttg ggcctcatta gcagggacct 540  
 ggtggatcgt caaaggaggt ttggttggga agacttggtc aanatttngg aanttaagtt 600  
 gtccnnnaac tngcgggggg gggnnnnnnn nnttnccant tccctncccc cngtttttng 660  
 nt 662

<210> 24  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> 105  
 <223> Xaa = Any Amino Acid

<400> 24  
 Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg  
 1 5 10 15  
 Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp  
 20 25 30  
 Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys  
 35 40 45  
 Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys  
 50 55 60  
 Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu  
 65 70 75 80  
 Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu  
 85 90 95  
 Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro  
 100 105 110  
 Ile Arg Asn Thr Gly Thr Phe  
 115

<210> 25  
 <211> 207  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide  
 <221> misc\_feature  
 <222> 112, 148, 158, 171, 178, 182, 191, 194, 203, 204  
 <223> n = A,T,C or G

<400> 25  
 ccctccctcc tgccgctcct ctctagaacc ttctagaacc tgggctgtgc tgctttttgag 60  
 cctcagaccc cagggcagca tctcggttct gcgccacttc ctttgtgttt anatggcggt 120  
 ttgtctgtgt tgctgttttag agtagatnaa ctgttttanat aaaaaaaaaa naaaattnac 180  
 tngagggggc ntgnaggcat gcnaac 207

<210> 26  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 26  
 gaagaggcaa gacgcttgta c

21

<210> 27  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 27

gtacaagcgt cttgcctctt c 21

<210> 28  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 28  
 gagtttgagc agatgttta 19

<210> 29  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<221> misc\_feature  
 <222> 3, 9, 15  
 <223> n = A,T,C or G

<400> 29  
 ggnaargcnc ayccncargc 20

<210> 30  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<221> misc\_feature  
 <222> 3, 6, 21  
 <223> n = A,T,C or G

<400> 30  
 atngcnggrt aytgytgdat ntc 23

<210> 31  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 31  
 grgayttraw bgabgchyam gawtgg 26

<210> 32  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;400&gt; 32

caagcbtggg aymtymtyta ytatmaygtb ttcag

35

&lt;210&gt; 33

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;400&gt; 33

gayybgartt ggctgtbcch gg

22

&lt;210&gt; 34

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

atgtccgtac	aagtagaaac	catctcccca	ggagacgggc	gcaccttccc	caagcgcggc	60
cagacctgcg	tggtgcacta	caccgggatg	cttgaagatg	gaaagaaatt	tgattcctcc	120
cgtgaccgta	acaagccctt	taagtttatg	ctaggcaagc	aggaggtgat	ccgaggctgg	180
gaagaagggg	ttgcccagat	gagtgtgggt	cagcgtgcc	aactgactat	atctccagat	240
tatgcctatg	gtgccactgg	gcacccaggc	atcatccac	cacatgccac	tctcgtcttc	300
gatgtggagc	ttctaaaact	ggaatga				327

&lt;210&gt; 35

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;400&gt; 35

gagatctgga attcggatcc tcgagagatc t

31